

Application No. 10/666,642

Amendment dated July 27, 2005

Reply to Restriction Requirement of June 30, 2005

**Amendments to the Claims:**

This listing of claims will replace all prior versions and listings of claims in the application.

**Listing of Claims:**

Claims 1-20 (canceled)

Claim 21 (new): A transgenic plant transformed with an expression vector comprising a polynucleotide sequence encoding a polypeptide having a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 22 (new): The transgenic plant of claim 21, wherein the expression vector further comprises a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide sequence.

Claim 23 (new): Seed produced by the transgenic plant according to claim 21, wherein the seed comprises the polynucleotide sequence of claim 21.

Claim 24 (new): A method for producing a transgenic plant having an altered trait as compared to a wild-type plant of the same species, the method steps comprising:

(a) providing an expression vector comprising:

(i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194; and

(ii) at least one regulatory element operably linked to the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;

(b) introducing the expression vector into at least one plant; and

(c) selecting at least one transgenic plant that has an altered trait as compared to a wild-type plant of the same species;

wherein the altered trait is selected from the group consisting of greater tolerance to cold during germination, greater tolerance to cold during growth, greater tolerance to drought, greater tolerance to nitrogen limitation, larger leaves, and greater biomass than the wild-type plant.

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Claim 25 (new): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least 75% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 26 (new): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 27 (new): The method of claim 24, wherein the regulatory element is a cauliflower mosaic virus 35S promoter.

Claim 28 (new): The method of claim 24, wherein the regulatory element is a root-specific, epidermis-specific, meristem-specific, or leaf-specific promoter.

Claim 29 (new): The method of claim 24, wherein the regulatory element is a drought-inducible or cold-inducible promoter.

Claim 30 (new): The method of claim 24, wherein the polypeptide comprises a DNA-binding domain combined with a GAL4 activation domain.

Claim 31 (new): The method of claim 24, wherein the transgenic plant has greater tolerance to 168 hours without watering than the wild-type plant.

Claim 32 (new): The method of claim 24, wherein the transgenic plant has greater tolerance than the wild-type plant to six hours of exposure to 8° C during germination or six hours of exposure to 4° to 8° C during growth.

Claim 33 (new): The method of claim 24, wherein the transgenic plant has greater tolerance than the wild-type plant to MS media with the nitrogen source reduced to 20 mg/l of NH<sub>4</sub>NO<sub>3</sub>.

Claim 34 (new): Seed produced by a transgenic plant produced by the method according to claim 24, wherein the seed comprises the expression vector of claim 24.

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**Claim 35 (new):** A method for increasing the tolerance of a plant to an abiotic stress, the method steps comprising:

- (a) providing an expression vector comprising:
  - (i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194; and
  - (ii) at least one regulatory element flanking the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;
- (b) introducing the expression vector into a plant, thereby producing a transgenic plant; and
- (c) selecting a transgenic plant having an altered trait as compared to a wild-type plant of the same species;  
wherein the abiotic stress is selected from the group consisting of cold stress during germination, cold stress during growth, drought stress, and nitrogen limitation.

**Claim 36 (new):** The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least 75% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

**Claim 37 (new):** The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

**Claim 38 (new):** The method of claim 35, wherein the transgenic plant has greater tolerance to 168 hours without watering than the wild-type plant.

**Claim 39 (new):** The method of claim 35, wherein the transgenic plant has greater tolerance than the wild-type plant to six hours of exposure to 8° C during germination or six hours of exposure to 4° to 8° C during growth.

**Claim 40 (new):** The method of claim 35, wherein the transgenic plant has greater tolerance than the wild-type plant to MS media with the nitrogen source reduced to 20 mg/l of NH<sub>4</sub>NO<sub>3</sub>.